Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-17. (Canceled)

18. (Original) A method for identifying and quantifying the presence of the fungus *Stachybotrys chartarum* in a collected sample, comprising:

obtaining a primer set and probe that is specific for the fungal species *Stachybotrys chartarum*;

collecting the sample from the environment;

extracting the sample's DNA;

obtaining DNA standards from a culture of *Stachybotrys chartarum*;

determining the concentration of *Stachybotrys chartarum* spores in the DNA standards;

amplifying by polymerase chain reaction each of the DNA standards and the collected sample's DNA using the obtained primer set and probe; and

comparing amplification plots obtained by polymerase chain reaction of each of the DNA standards and the collected sample's DNA to obtain an indication of the presence of the fungus *Stachybotrys chartarum* in the collected sample and a concentration of the fungus *Stachybotrys chartarum* in the collected sample.

19. (New) The method of claim 18, wherein the primer set and probe comprises:

a forward primer comprising a base sequence (SEQ ID NO: 1) 5'GTTGCTTCGGCGGGAAC3';

a reverse primer comprising a base sequence (SEQ ID NO: 2) 5'TTTGCGTTTGCCACTCAGAG3'; and

a probe comprising a base sequence (SEQ ID NO: 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAMRA.

20. (New) The method of claim 18, wherein the primer set and probe comprises:

a forward primer comprising a base sequence (SEQ ID NO: 3) 5'ACCTATCGTTGCTTCGGCG3';

a reverse primer comprising a base sequence (SEQ ID NO: 4) 5'GCGTTTGCCACTCAGAGAATACT3'; and

a probe comprising a base sequence (SEQ ID NO 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAMRA.

21. (New) The method of claim 18, wherein the concentration of *Stachybotrys chartarum* spores in the DNA standards is determined via direct total count of the *Stachybotrys chartarum* spores in the DNA standards.

22. (New) A method for identifying and quantifying the presence of the fungus *Stachybotrys chartarum* in a collected sample, comprising:

obtaining a primer set and probe that is specific for the fungal species *Stachybotrys chartarum*,

wherein the obtained primer set and probe comprises:

a forward primer comprising a base sequence (SEQ ID NO: 1) 5'GTTGCTTCGGCGGGAAC3';

a reverse primer comprising a base sequence (SEQ ID NO: 2) 5'TTTGCGTTTGCCACTCAGAG3'; and

a probe comprising a base sequence (SEQ ID NO: 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAMRA; and

employing quantitative polymerase chain reaction, using the obtained primer and probe set, to determine a concentration of the fungus *Stachybotrys chartarum* in the collected sample.

23. (New) The method of claim 22, wherein employing quantitative polymerase chain reaction further comprises:

extracting the collected sample's DNA;

obtaining one or more DNA standards from a culture of *Stachybotrys chartarum*;

determining a concentration of *Stachybotrys chartarum* spores in each of the one or more DNA standards;

amplifying by polymerase chain reaction each of the one or more DNA standards and the collected sample's DNA using the obtained primer set and probe; and

comparing amplification plots obtained by polymerase chain reaction of each of the one or more DNA standards and the collected sample's DNA to determine the concentration of the fungus *Stachybotrys chartarum* in the collected sample.

24. (New) The method of claim 23, wherein the concentration of *Stachybotrys chartarum* spores in each of the one or more DNA standards is determined via direct total count of the *Stachybotrys chartarum* spores in the DNA standards.

25. (New) A method for identifying and quantifying the presence of the fungus *Stachybotrys chartarum* in a collected sample, comprising:

obtaining a primer set and probe that is specific for the fungal species *Stachybotrys chartarum*,

wherein the obtained primer set and probe comprises:

a forward primer comprising a base sequence (SEQ ID NO: 3) 5'ACCTATCGTTGCTTCGGCG3';

a reverse primer comprising a base sequence (SEQ ID NO: 4) 5'GCGTTTGCCACTCAGAGAATACT3'; and

a probe comprising a base sequence (SEQ ID NO: 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAM; and

employing quantitative polymerase chain reaction, using the obtained primer and probe set, to determine a concentration of the fungus *Stachybotrys chartarum* in the collected sample.

26. (New) The method of claim 25, wherein employing quantitative polymerase chain reaction further comprises:

extracting the collected sample's DNA;

obtaining one or more DNA standards from a culture of *Stachybotrys chartarum*;

determining a concentration of *Stachybotrys chartarum* spores in each of the one or more DNA standards;

amplifying by polymerase chain reaction each of the one or more DNA standards and the collected sample's DNA using the obtained primer set and probe; and

comparing amplification plots obtained by polymerase chain reaction of each of the one or more DNA standards and the collected sample's DNA to determine the concentration of the fungus *Stachybotrys chartarum* in the collected sample.

27. (New) The method of claim 26, wherein the concentration of *Stachybotrys chartarum* spores in each of the one or more DNA standards is determined via direct total count of the *Stachybotrys chartarum* spores in the DNA standards.